#### SEQUENCE LISTING

- (1) GENERAL INFORMATION:
  - (i) APPLICANT: KOLTERMAN, Orville G.
    YOUNG, Andrew A.
    RINK, Timothy J.
    BROWN, Kathleen Ann Keiting
  - (ii) TITLE OF INVENTION: METHODS FOR REGULATING
    GASTROINTESTINAL MOTILITY
  - (iii) NUMBER OF SEQUENCES: 30
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    - (E) COUNTRY: USA
    - (F) ZIP: 90017
    - (v) COMPUTER READABLE FORM:
      - (A) MEDIUM TYPE: Floppy disk
      - (B) COMPUTER: IBM PC compatible
      - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
      - (D) SOFTWARE: PatentIn Release #1.0, Version #1.25
    - (vi) CURRENT APPLICATION DATA:
      - (A) APPLICATION NUMBER: 08/302,069
      - (B) FILING DATE: 07-SEP-1994
        - (C) CLASSIFICATION: Pending
  - (vii) PRIOR APPLICATION DATA:
    - (A) APPLICATION NUMBER: 08/118,381
    - (B) FILING DATE: 07-SEP-1993
  - (viii) ATTORNEY/AGENT INFORMATION:
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- (2) INFORMATION FOR SEQ ID NO:1:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 37 amino acids

- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
  - (B) LOCATION: 2,7
  - (D) OTHER INFORMATION: disulfide bridge between the Cys residues
  - (B) LOCATION: 37
  - (D) OTHER INFORMATION: amidated Tyr (Tyrosinamide)
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

Lys Cys Asn Thr Ala Thr Cys Ala Thr Gln Arg Leu Ala Asn Phe Leu

1. 5 10 15

Val His Ser Ser Asn Asn Phe Gly Pro Ile Leu Pro Pro Ihr Asn Val
20 25 30

Gly Ser Asn Thr Tyr
35

- (2) INFORMATION FOR SEQ ID NO:2:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 24 amino acids
    - (B) TYPE: amino acids
    - (C) STRANDEDNESS: single
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: peptide
    - (ix) FEATURE:
      - (B) LOCATION: 24
      - (D) OTHER INFORMATION: amidated Tyr (Tyrosinamide)
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Leu Gly Arg Leu Ser Gln Glu Leu His Arg Leu Gln Thr Tyr Pro Arg

1 5 10 15

Thr Asn Thr Gly Ser Asn Thr Tyr
20

- (2) INFORMATION FOR SEQ ID NO:3:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 37 amino acids
    - (B) TYPE: amino acid

- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: peptide

- (ix) FEATURE:
  - (B) LOCATION: 2,7
  - (D) OTHER INFORMATION: disulfide bridge between

the Cys residues

- (B) LOCATION: 37
- (D) OTHER INFORMATION: amidated Tyr (Tyrosinamide)
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

### (2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 36 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
  - (ix) FEATURE:
    - (B) LOCATION: 1,6
    - (D) OTHER INFORMATION: disulfide bridge between

the Cys residues

- (B) LOCATION: 36
- (D) OTHER INFORMATION: amidated Tyr (Tyrosinamide)
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Cys Asn Thr Ala Thr Cys Ala Thr Gln Arg Leu Ala Asn Phe Leu Val 1 10 15

His Ser Ser Asn Asn Phe Gly Ala Ile Leu Ser Ser Thr Asn Val Gly 20 25 30

Ser Asn Thr Tyr

SD-111162.1

- (2) INFORMATION FOR SEQ ID NO:5:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 37 amino acids
    - (B) TYPE: amino acid
    - (C) STRANDEDNESS: single
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: peptide
  - (ix) FEATURE:
    - (B) LOCATION: 2,7
    - (D) OTHER INFORMATION: disulfide bridge between the Cys residues
    - (B) LOCATION: 37
      - (D) OTHER INFORMATION: amidated Tyr (Tyrosinamide)
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

- (2) INFORMATION FOR SEQ ID NO:6:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 36 amino acids
      - (B) TYPE: amino acid
      - (C) STRANDEDNESS: single
      - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: peptide
  - (ix) FEATURE:
    - (B) LOCATION: 1,6
    - (D) OTHER INFORMATION: disulfide bridge between the Cys residues
    - (B) LOCATION: 36
    - (D) OTHER INFORMATION: amidated Tyr (Tyrosinamide)
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Cys Asn Thr Ala Thr Cys Ala Thr Gln Arg Leu Ala Asn Phe Leu Val 1 5 10 15 sp-111162.1 Arg Ser Ser Asn Asn Phe Gly Pro Ile Leu Pro Ser Thr Asn Val Gly
20 25 30
Ser Asn Thr Tyr
35

- (2) INFORMATION FOR SEQ ID NO:7:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 37 amino acids
    - (B) TYPE: amino acid
    - (C) STRANDEDNESS: single
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: peptide
  - (ix) FEATURE:
    - (B) LOCATION: 2,7
    - (D) OTHER INFORMATION: disulfide bridge between the Cys residues
    - (B) LOCATION: 37
    - (D) OTHER INFORMATION: amidated Tyr (Tyrosinamide)
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Lys Cys Asn Thr Ala Thr Cys Ala Thr Gln Arg Leu Ala Asn Phe Leu

1 5 10 15

Val His Ser Ser Asn Asn Phe Gly Pro Val Leu Pro Pro Thr Asn Val

20 25 30

Gly Ser Asn Thr Tyr

35

- (2) INFORMATION FOR SEQ ID NO:8:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 37 amino acids
    - (B) TYPÉ: amino acid
    - (C) STRANDEDNESS: single
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: peptide
  - (ix) FEATURE:
    - (B) LOCATION: 2,7
    - (D) OTHER INFORMATION: disulfide bridge between the Cys residues

- (B) LOCATION: 37
- (D) OTHER INFORMATION: amidated Tyr (Tyrosinamide)
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Lys Cys Asn Thr Ala Thr Cys Ala Thr Gln Arg Leu Ala Asn Phe Leu 1 10 15

Val Arg Ser Ser Asn Asn Phe Gly Pro Ile Leu Pro Pro Thr Asn Val 20 25 30

Gly Ser Asn Thr Tyr 35

- (2) INFORMATION FOR SEQ ID NO:9:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 36 amino acids
    - (B) TYPE: amino acid
    - (C) STRANDEDNESS: single
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: peptide
    - (ix) FEATURE:
      - (B) LOCATION: 1,6
      - (D) OTHER INFORMATION: disulfide bridge between
        - the Cys residues
      - (B) LOCATION: 36
      - (D) OTHER INFORMATION: amidated Tyr (Tyrosinamide)
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

Cys Asn Thr Ala Thr Cys Ala Thr Gln Arg Leu Ala Asn Phe Leu Val 1 5 10 15 Arg Ser Ser Asn Asn Phe Gly Pro Ile Leu Pro Pro Thr Asn Val Gly 20 25 30 Ser Asn Thr Tyr 35

- (2) INFORMATION FOR SEQ ID NO:10:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 36 amino acids
    - (B) TYPE: amino acid

- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
  - (B) LOCATION: 1,6
  - (D) OTHER INFORMATION: disulfide bridge between the Cys residues
  - (B) LOCATION: 36
  - (D) OTHER INFORMATION: amidated Tyr (Tyrosinamide)
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Cys Asn Thr Ala Thr Cys Ala Thr Gln Arg Leu Ala Asn Phe Leu Val 1 5 10 15 His Ser Ser Asn Asn Phe Gly Pro Ile Leu Pro Pro Thr Asn Val Gly 20 25 30 Ser Asn Thr Tyr

- (2) INFORMATION FOR SEQ ID NO:11:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 37 amino acids
    - (B) TYPE: amino acid
    - (C) STRANDEDNESS: single
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: peptide
    - (ix) FEATURE:
      - (B) LOCATION: 2,7
      - (D) OTHER INFORMATION: disulfide bridge between the Cys residues
      - (B) LOCATION: 37
      - (D) OTHER INFORMATION: amidated Tyr (Tyrosinamide)
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

Lys Cys Asn Thr Ala Thr Cys Ala Thr Gln Arg Leu Ala Asn Phe Leu 1 5 10 15 Val His Ser Ser Asn Asn Leu Gly Pro Val Leu Pro Pro Thr Asn Val 20 25 30 Gly Ser Asn Thr Tyr 35

- (2) INFORMATION FOR SEQ ID NO:12:
  - (i) SEQUENCE CHARACTERISTICS:

    (A) LENGTH: 37 amino acids

- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: peptide

- (ix) FEATURE:
  - (B) LOCATION: 2,7
  - (D) OTHER INFORMATION: disulfide bridge between the Cys residues
  - (B) LOCATION: 37
  - (D) OTHER INFORMATION: amidated Tyr (Tyrosinamide)
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

Lys Cys Asn Thr Ala Thr Cys Ala Thr Gln Arg Leu Ala Asn Phe Leu

1 5 10 15

Val His Ser Ser Asn Asn Leu Gly Pro Val Leu Pro Ser Thr Asn Val
20 25 30

Gly Ser Asn Thr Tyr
35

### (2) INFORMATION FOR SEQ ID NO:13:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 36 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
  - (ix) FEATURE:
    - (B) LOCATION: 1,6
    - (D) OTHER INFORMATION: disulfide bridge between the Cys residues
    - (B) LOCATION: 36
    - (D) OTHER INFORMATION: amidated Tyr (Tyrosinamide)
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

Cys Asn Thr Ala Thr Cys Ala Thr Gln Arg Leu Ala Asn Phe Leu Val 1 5 10 15 His Ser Ser Asn Asn Leu Gly Pro Val Leu Pro Ser Thr Asn Val Gly 20 25 30 Ser Asn Thr Tyr 35

- (2) INFORMATION FOR SEQ ID NO:14:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 37 amino acids
    - (B) TYPE: amino acid
    - (C) STRANDEDNESS: single
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: protein
    - (ix) FEATURE:
      - (B) LOCATION: 2,7
      - (D) OTHER INFORMATION: disulfide bridge between the Cys residues
      - (B) LOCATION: 37
      - (D) OTHER INFORMATION: amidated Tyr (Tyrosinamide)
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

Lys Cys Asn Thr Ala Thr Cys Ala Thr Gln Arg Leu Ala Asn Phe Leu 1 5 10 15

Val Arg Ser Ser Asn Asn Leu Gly Pro Val Leu Pro Ser Thr Asn Val 20 25 30

Gly Ser Asn Thr Tyr 35

- (2) INFORMATION FOR SEQ ID NO:15:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 37 amino acids
    - (B) TYPE: amino acid
    - (C) STRANDEDNESS: single
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: protein
  - (ix) FEATURE:
    - (B) LOCATION: 2,7
    - (D) OTHER INFORMATION: disulfide bridge between the Cys residues
    - (B) LOCATION: 37
    - (D) OTHER INFORMATION: amidated Tyr (Tyrosinamide)
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

- (2) INFORMATION FOR SEQ ID NO:16:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 37 amino acids
    - (B) TYPE: amino acid
    - (C) STRANDEDNESS: single
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: protein
  - (ix) FEATURE:
    - (B) LOCATION: 2,7
  - (D) OTHER INFORMATION: disulfide bridge between the Cys residues
    - (B) LOCATION: 37
    - (D) OTHER INFORMATION: amidated Tyr (Tyrosinamide)
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

Lys Cys Asn Thr Ala Thr Cys Ala Thr Gln Arg Leu Ala Asn Phe Leu 1 10 15

Val Arg Ser Ser Asn Asn Leu Gly Pro Ile Leu Pro Ser Thr Asn Val 20 25 30

Gly Ser Asn Thr Tyr 35

- (2) INFORMATION FOR SEQ ID NO:17:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 37 amino acids
    - (B) TYPE: amino acid
    - (C) STRANDEDNESS: single
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: protein
  - (ix) FEATURE:
    - (B) LOCATION: 2,7
    - (D) OTHER INFORMATION: disulfide bridge between the Cys residues
    - (B) LOCATION: 37
    - (D) OTHER INFORMATION: amidated Tyr (Tyrosinamide)
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

Lys Cys Asn Thr Ala Thr Cys Ala Thr Gln Arg Leu Ala Asn Phe Leu 1 5 10 15

Ile His Ser Ser Asn Asn Leu Gly Pro Ile Leu Pro Pro Thr Asn Val 20 25 30 Gly Ser Asn Thr Tyr 35

- (2) INFORMATION FOR SEQ ID NO:18:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 37 amino acids
    - (B) TYPE: amino acid
    - (C) STRANDEDNESS: single
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: protein
  - (ix) FEATURE:
    - (B) LOCATION: 2,7
      - (D) OTHER INFORMATION: disulfide bridge between the Cys residues
      - (B) LOCATION: 37
      - (D) OTHER INFORMATION: amidated Tyr (Tyrosinamide)
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

Lys Cys Asn Thr Ala Thr Cys Ala Thr Gln Arg Leu Ala Asn Phe Leu 1 5 10 15

Ile His Ser Ser Asn Asn Phe Gly Pro Ile Leu Pro Pro Thr Asn Val 20 25 30

Gly Ser Asn Thr Tyr 35

- (2) INFORMATION FOR SEQ ID NO:19:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 36 amino acids
    - (B) TYPE: amino acid
    - (C) STRANDEDNESS: single
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: protein
  - (ix) FEATURE:
    - (B) LOCATION: 1,6
    - (D) OTHER INFORMATION: disulfide bridge between the Cys residues
    - (B) LOCATION: 36
    - (D) OTHER INFORMATION: amidated Tyr (Tyrosinamide)

### (xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

Cys Asn Thr Ala Thr Cys Ala Thr Gln Arg Leu Ala Asn Phe Leu Ile
1 5 10 15
His Ser Ser Asn Asn Leu Gly Pro Ile Leu Pro Pro Thr Asn Val Gly
20 25 30
Ser Asn Thr Tyr
35

#### (2) INFORMATION FOR SEQ ID NO:20:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 37 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (1i) MOLECULE TYPE: protein
  - (ix) FEATURE:
    - (B) LOCATION: 2,7
    - (D) OTHER INFORMATION: disulfide bridge between the Cys residues
    - (B) LOCATION: 37
    - (D) OTHER INFORMATION: amidated Tyr (Tyrosinamide)
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

#### (2) INFORMATION FOR SEQ ID NO:21:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 37 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein

## (ix) FEATURE:

- (B) LOCATION: 2,7
- (D) OTHER INFORMATION: disulfide bridge between the Cys residues
- (B) LOCATION: 37
- (D) OTHER INFORMATION: amidated Tyr (Tyrosinamide)
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

Lys Cys Asn Thr Ala Thr Cys Ala Thr Gln Arg Leu Ala Asn Phe Leu 1 5 10 15

Ile Arg Ser Ser Asn Asn Leu Gly Ala Val Leu Ser Pro Thr Asn Val 20 25 30

Gly Ser Asn Thr Tyr 35

# (2) INFORMATION FOR SEQ ID NO:22:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 37 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (ix) FEATURE:
  - (B) LOCATION: 2,7
  - (D) OTHER INFORMATION: disulfide bridge between the Cys residues
  - (B) LOCATION: 37
  - (D) OTHER INFORMATION: amidated Tyr (Tyrosinamide)
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

Lys Cys Asn Thr Ala Thr Cys Ala Thr Gln Arg Leu Ala Asn Phe Leu 1 5 5 10 10 15 15 15 16 Arg Ser Ser Asn Asn Leu Gly Pro Val Leu Pro Pro Thr Asn Val 20 25 30 30 Gly Ser Asn Thr Tyr 35

# (2) INFORMATION FOR SEQ ID NO:23:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 37 amino acids
  - (B) TYPE: amino acid

- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

# (ii) MOLECULE TYPE: protein

## (ix) FEATURE:

- (B) LOCATION: 2,7
- (D) OTHER INFORMATION: disulfide bridge between the Cys\_residues
- (B) LOCATION: 37
- (D) OTHER INFORMATION: amidated Tyr (Tyrosinamide)
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

Lys Cys Asn Thr Ala Thr Cys Ala Thr Gln Arg Leu Thr Asn Phe Leu 1 5 10 10 15

Val His Ser Ser His Asn Leu Gly Ala Ala Leu Leu Pro Thr Asp Val 20 25 30

Gly Ser Asn Thr Tyr 35

# (2) INFORMATION FOR SEQ ID NO:24:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 37 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (ix) FEATURE:
  - (B) LOCATION: 2,7
  - (D) OTHER INFORMATION: disulfide bridge between the Cys residues
  - (B) LOCATION: 37
  - (D) OTHER INFORMATION: amidated Tyr (Tyrosinamide)
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

- (2) INFORMATION FOR SEQ ID NO:25:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 36 amino acids
    - (B) TYPE: amino acid
    - (C) STRANDEDNESS: single
    - (D) TOPOLOGY: linear
    - (ii) MOLECULE TYPE: protein
      - (ix) FEATURE:
        - (B) LOCATION: 1,6
        - (D) OTHER INFORMATION: disulfide bridge between the Cys residues
        - (B) LOCATION: 36
        - (D) OTHER INFORMATION: amidated Tyr (Tyrosinamide)
    - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

- (2) INFORMATION FOR SEQ ID NO:26:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 37 amino acids
    - (B) TYPE: amino acid
    - (C) STRANDEDNESS: single
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: protein
    - (ix) FEATURE:
      - (B) LOCATION: 2,7
      - (D) OTHER INFORMATION: disulfide bridge between the Cys residues
      - (B) LOCATION: 37
      - (D) OTHER INFORMATION: amidated Tyr (Tyrosinamide)
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

Lys Cys Asn Thr Ala Thr Cys Ala Thr Gln Arg Leu Thr Asn Phe Leu 1 5 10 15

Val Arg Ser Ser His Asn Leu Gly Ala Ala Leu Ser Pro Thr Asp Val 20 25 30 Gly Ser Asn Thr Tyr 35

- (2) INFORMATION FOR SEQ ID NO:27:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 37 amino acids
    - (B) TYPE: amino acid
    - (C) STRANDEDNESS: single
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: protein
  - (ix) FEATURE:
    - (B) LOCATION: 2,7
    - (D) OTHER INFORMATION: disulfide bridge between the Cys residues
    - (B) LOCATION: 37
    - (D) OTHER INFORMATION: amidated Tyr (Tyrosinamide)
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

Lys Cys Asn Thr Ala Thr Cys Ala Thr Gln Arg Leu Thr Asn Phe Leu

1 10 15

Val Arg Ser Ser His Asn Leu Gly Ala Ile Leu Pro Pro Thr Asp Val
20 25 30

Gly Ser Asn Thr Tyr
35

- (2) INFORMATION FOR SEQ ID NO:28:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 37 amino acids
    - (B) TYPE: amino acid
    - (C) STRANDEDNESS: single
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: protein
  - (ix) FEATURE:
    - (B) LOCATION: 2,7
    - (D) OTHER INFORMATION: disulfide bridge between the Cys residues

- (B) LOCATION: 37
- (D) OTHER INFORMATION: amidated Tyr (Tyrosinamide)
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

- (2) INFORMATION FOR SEQ ID NO:29:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 25 amino acids
    - (B) TYPE: amino acid
    - (C) STRANDEDNESS: single
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: protein
  - (ix) FEATURE:
    - (B) LOCATION: 25
    - (D) OTHER INFORMATION: amidated Tyr (Tyrosinamide)
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

Val Leu Gly Lys Leu Ser Gln Glu Leu His Lys Leu Gln Thr Tyr Pro
1 5 10 15

Arg Thr Asn Thr Gly Ser Asn Thr Tyr
20 25

- (2) INFORMATION FOR SEQ ID NO:30:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 25 amino acids
    - (B) TYPE: amino acid
    - (C) STRANDEDNESS: single
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: protein
  - (ix) FEATURE:
    - (B) LOCATION: 25
    - (D) OTHER INFORMATION: amidated Pro (Prolinamide)
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:30: SD-111162.1

Val Leu Gly Lys Leu Ser Gln Glu Leu His Lys Leu Gln Thr Tyr Pro 1 5 5 10 15 15
Arg Thr Asn Thr Gly Ser Gly Thr Pro 20 25